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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/932,367A

DATE: 02/13/2002

TIME: 18:44:29

Input Set : A:\053844-5003.txt

Output Set: N:\CRF3\02132002\I932367A.raw

ENTERED
see page 5

3 <110> APPLICANT: RHODES, Simon J.
 4 BRIDWELL, Jeanne L.
 5 MEIER, Bradley C.
 6 PARKER, Gretchen E.
 7 PRICE, Jeffrey R.
 8 SHOWALTER, Aaron D.
 9 SLOOP, Kyle W.
 11 <120> TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN
 12 LHX3/P-LIM/LIM-3 FACTOR
 14 <130> FILE REFERENCE: 053844-5003
 16 <140> CURRENT APPLICATION NUMBER: 09/932,367A
 17 <141> CURRENT FILING DATE: 2001-08-17
 19 <150> PRIOR APPLICATION NUMBER: PCT/US00/04424
 20 <151> PRIOR FILING DATE: 2000-02-22
 22 <150> PRIOR APPLICATION NUMBER: US 60/121,110
 23 <151> PRIOR FILING DATE: 1999-02-22
 25 <160> NUMBER OF SEQ ID NOS: 113
 27 <170> SOFTWARE: PatentIn Ver. 2.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 1605
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Sus scrofa
 34 <400> SEQUENCE: 1
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 36 ccagcacatc ctggaccgct tcatcctcaa ggctctggac cgccactgac acagcaagtg 120
 37 cctcaagtgc agtgactgcc acacggcgct ggccgagcgc tgcttcagcc gcggagagag 180
 38 cctctactgc aaggacgact tcttcaagcg cttcgggacc aagtgcgcgg cgtgccagct 240
 39 gggcatcccg cccacgcagg tggtgccgcg cgccccaggac ttctgttacc acctgcactg 300
 40 cttcgccctgc gtcgtgtgca agcggcagct ggccacgggc gacgagttct acctcatgg 360
 41 ggacagccgg ctcgtgtgca aggccgacta cgagaccggc aagcagcggag aggccgaggc 420
 42 cacggccaag cggccgcgcgca cgaccatcac ggccaaggcag ctggagacgc tgaagagcgc 480
 43 ctacaacacg tcgcccaagc cccgcgcgcgc cgtgcgcgag cagtcctctt ccggagaccgg 540
 44 cctggacatg cgcgtcgtgc agtgtgtgtt ccagaaccgc cggggccaagg aaaagcggct 600
 45 caagaaggac gccggccggc agcgctgggg ccagtacttt cgtaacataga agcgcgcggc 660
 46 cggggctcc aagtccggaca aggacagcgt ccaggaggag gggcaggaca gtacgcgcga 720
 47 ggtctcccttc acagacgacg catccatggc cggaaatgggc cctgccaacg gcctctacgg 780
 48 cggcctgggg gaggcctgccc ctgccttggg cccgcctcg gggggccccc gcagcttccc 840
 49 gctggagcac ggaggcctgg cggggccggc gcagtatggc gagctgcgcgc ccagcagcc 900
 50 ctacgggtgc ccctcgctgc cccgcgcctc gcagagcctc cctggccccc agccctctt 960
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 52 gccccccaccc atgagggtgc tggcaggaa cggaccgc tccgacatcat ccacggggag 1080
 53 cagtgggggc taccccgact tcctgcac tccgcctcc tggctggacg aggtggatca 1140
 54 cgctcagttc tgactgaggc cccagctccg tggagcacca gacacgagca ctgcccctgg 1200

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55 ctgggtggtc gggagccgcg ctctccttgc ccgaagccct gggcctctaa aggacacagg 1260
 56 gtcaccggcg gggcacaggc tgaggactgt ccagccgcg gcgcctggcc cgggcagag 1320
 57 ggactttctc ccggtctcga ggctccttgc gggacaaggg gagccacctg gtggctgctc 1380
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 59 gctgctctt cttagaccgga gtggtcagcc cccgaagccg gggagggggg ctctccccag 1500
 60 cccagagcag cacagccctc agactggaag atgcttaat tttaaaatt aaaaaataat 1560
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 65 <211> LENGTH: 383
 66 <212> TYPE: PRT
 67 <213> ORGANISM: Sus scrofa
 69 <400> SEQUENCE: 2
 70 Trp Glu Gly Arg Pro Gln Glu Leu Gly Gly Lys Glu Ile Pro Leu Cys
 71 1 5 10 15
 73 Ala Gly Cys Asp Gln His Ile Leu Asp Arg Phe Ile Leu Lys Ala Leu
 74 20 25 30
 76 Asp Arg His Trp His Ser Lys Cys Leu Lys Cys Ser Asp Cys His Thr
 77 35 40 45
 79 Pro Leu Ala Glu Arg Cys Phe Ser Arg Gly Glu Ser Leu Tyr Cys Lys
 80 50 55 60
 82 Asp Asp Phe Phe Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys Gln Leu
 83 65 70 75 80
 85 Gly Ile Pro Pro Thr Gln Val Val Arg Arg Ala Gln Asp Phe Val Tyr
 86 85 90 95
 88 His Leu His Cys Phe Ala Cys Val Val Cys Lys Arg Gln Leu Ala Thr
 89 100 105 110
 91 Gly Asp Glu Phe Tyr Leu Met Glu Asp Ser Arg Leu Val Cys Lys Ala
 92 115 120 125
 94 Asp Tyr Glu Thr Ala Lys Gln Arg Glu Ala Glu Ala Thr Ala Lys Arg
 95 130 135 140
 97 Pro Arg Thr Thr Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys Ser Ala
 98 145 150 155 160
 100 Tyr Asn Thr Ser Pro Lys Pro Ala Arg His Val Arg Glu Gln Leu Ser
 101 165 170 175
 103 Ser Glu Thr Gly Leu Asp Met Arg Val Val Gln Val Trp Phe Gln Asn
 104 180 185 190
 106 Arg Arg Ala Lys Glu Lys Arg Leu Lys Lys Asp Ala Gly Arg Gln Arg
 107 195 200 205
 109 Trp Gly Gln Tyr Phe Arg Asn Met Lys Arg Ala Arg Gly Gly Ser Lys
 110 210 215 220
 112 Ser Asp Lys Asp Ser Val Gln Glu Glu Gly Gln Asp Ser Asp Ala Glu
 113 225 230 235 240
 115 Val Ser Phe Thr Asp Glu Pro Ser Met Ala Glu Met Gly Pro Ala Asn
 116 245 250 255
 118 Gly Leu Tyr Gly Gly Leu Gly Glu Pro Ala Pro Ala Leu Gly Arg Pro
 119 260 265 270
 121 Ser Gly Ala Pro Gly Ser Phe Pro Leu Glu His Gly Gly Leu Ala Gly
 122 275 280 285
 124 Pro Glu Gln Tyr Gly Glu Leu Arg Pro Ser Ser Pro Tyr Gly Val Pro

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Input Set : A:\053844-5003.txt
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125 290 295 300
 127 Ser Ser Pro Ala Ala Leu Gln Ser Leu Pro Gly Pro Gln Pro Leu Leu
 128 305 310 315 320
 130 Ser Ser Leu Val Tyr Pro Glu Ala Gly Leu Gly Leu Val Pro Ala Gly
 131 325 330 335
 133 Pro Pro Gly Gly Pro Pro Pro Met Arg Val Leu Ala Gly Asn Gly Pro
 134 340 345 350
 136 Ser Ser Asp Leu Ser Thr Gly Ser Ser Gly Gly Tyr Pro Asp Phe Pro
 137 355 360 365
 139 Ala Ser Pro Ala Ser Trp Leu Asp Glu Val Asp His Ala Gln Phe
 140 370 375 380
 143 <210> SEQ ID NO: 3
 144 <211> LENGTH: 399
 145 <212> TYPE: PRT
 146 <213> ORGANISM: Mus musculus
 148 <400> SEQUENCE: 3
 149 Met Leu Leu Glu Ala Glu Leu Asp Cys His Arg Glu Arg Pro Gly Ala
 150 1 5 10 15
 152 Pro Gly Ala Ser Ala Leu Cys Thr Phe Ser Arg Thr Pro Glu Ile Pro
 153 20 25 30
 155 Met Cys Ala Gly Cys Asp Gln His Ile Leu Asp Arg Phe Ile Leu Lys
 156 35 40 45
 158 Ala Leu Asp Arg His Trp His Ser Lys Cys Leu Lys Cys Ser Asp Cys
 159 50 55 60
 161 His Val Pro Leu Ala Glu Arg Cys Phe Ser Arg Gly Glu Ser Val Tyr
 162 65 70 75 80
 164 Cys Lys Asp Asp Phe Phe Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys
 165 85 90 95
 167 Gln Leu Gly Ile Pro Pro Thr Gln Val Val Arg Arg Ala Gln Asp Phe
 168 100 105 110
 170 Val Tyr His Leu His Cys Phe Ala Cys Val Val Cys Lys Arg Gln Leu
 171 115 120 125
 173 Ala Thr Gly Asp Glu Phe Tyr Leu Met Glu Asp Ser Arg Leu Val Cys
 174 130 135 140
 176 Lys Ala Asp Tyr Glu Thr Ala Lys Gln Arg Glu Ala Glu Ala Thr Ala
 177 145 150 155 160
 179 Lys Arg Pro Arg Thr Thr Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys
 180 165 170 175
 182 Ser Ala Tyr Asn Thr Ser Pro Lys Pro Ala Arg His Val Arg Glu Gln
 183 180 185 190
 185 Leu Ser Ser Glu Thr Gly Leu Asp Arg Val Val Gln Val Trp Phe Gln
 186 195 200 205
 188 Asn Arg Arg Ala Lys Glu Lys Arg Leu Lys Lys Asp Ala Gly Arg Gln
 189 210 215 220
 191 Arg Trp Gly Gln Tyr Phe Arg Asn Met Lys Arg Ser Arg Gly Ser Ser
 192 225 230 235 240
 194 Lys Ser Asp Lys Asp Ser Ile Gln Glu Gly Gln Asp Ser Asp Ala Glu
 195 245 250 255
 197 Val Ser Phe Thr Asp Glu Pro Ser Met Ala Asp Met Gly Pro Ala Asn

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198 260 265 270
 200 Gly Leu Tyr Ser Ser Leu Gly Glu Pro Ala Pro Ala Leu Gly Arg Pro
 201 275 280 285
 203 Val Gly Gly Leu Gly Ser Phe Thr Leu Asp His Gly Gly Leu Thr Gly
 204 290 295 300
 206 Pro Glu Gln Tyr Arg Glu Leu Arg Pro Gly Ser Pro Tyr Gly Ile Pro
 207 305 310 315 320
 209 Pro Ser Pro Ala Ala Pro Gln Ser Leu Pro Gly Pro Gln Pro Leu Leu
 210 325 330 335
 212 Ser Ser Leu Val Tyr Pro Asp Thr Asn Leu Ser Leu Val Pro Ser Gly
 213 340 345 350
 215 Pro Pro Gly Gly Pro Pro Met Arg Val Leu Ala Gly Asn Gly Pro
 216 355 360 365
 218 Ser Ser Asp Leu Ser Thr Glu Ser Ser Ser Gly Tyr Pro Asp Phe Pro
 219 370 375 380
 221 Ala Ser Pro Ala Ser Trp Leu Asp Glu Val Asp His Ala Gln Phe
 222 385 390 395
 225 <210> SEQ ID NO: 4
 226 <211> LENGTH: 395
 227 <212> TYPE: PRT
 228 <213> ORGANISM: Gallus gallus
 230 <400> SEQUENCE: 4
 231 Met Leu Leu Glu Arg Val Arg Ala Gly Ser Glu Lys Ala Ala Glu Leu
 232 1 5 10 15
 234 Cys Pro Phe Pro Arg Ser Pro Glu Ile Pro Leu Cys Ala Gly Cys Asn
 235 20 25 30
 237 Gln His Ile Val Asp Arg Phe Ile Leu Lys Val Leu Asp Arg His Trp
 238 35 40 45
 240 His Ser Lys Cys Leu Lys Cys Ser Asp Cys Gln Thr Gln Leu Ala Glu
 241 50 55 60
 243 Lys Cys Phe Ser Arg Gly Asp Gly Val Tyr Cys Lys Glu Asp Phe Phe
 244 65 70 75 80
 246 Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys Gln Gln Gly Ile Pro Pro
 247 85 90 95
 249 Thr Gln Val Val Arg Arg Ala Gln Asp Phe Val Tyr His Leu His Cys
 250 100 105 110
 252 Phe Ala Cys Ile Val Cys Lys Arg Gln Leu Ala Thr Gly Asp Glu Phe
 253 115 120 125
 255 Tyr Leu Met Glu Asp Ser Arg Leu Val Cys Lys Ala Asp Tyr Glu Thr
 256 130 135 140
 258 Ala Lys Gln Arg Glu Ala Glu Ser Thr Ala Lys Arg Pro Arg Thr Thr
 259 145 150 155 160
 261 Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys Asn Ala Tyr Asn Asn Ser
 262 165 170 175
 264 Pro Lys Pro Ala Arg His Val Arg Glu Gln Leu Ser Ser Glu Thr Gly
 265 180 185 190
 267 Leu Asp Met Arg Val Val Gln Val Trp Phe Gln Asn Arg Arg Ala Lys
 268 195 200 205
 270 Glu Lys Arg Leu Lys Lys Asp Ala Gly Arg Gln Arg Trp Gly Gln Tyr

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271 210 215 220
 273 Phe Arg Asn Met Lys Arg Ser Arg Gly Thr Ser Lys Ser Asp Lys Asp
 274 225 230 235 240
 276 Ser Ile Gln Glu Glu Gly Pro Asp Ser Asp Ala Glu Val Ser Phe Thr
 277 245 250 255
 279 Asp Glu Pro Ser Met Ser Glu Met Ser His Ser Asn Gly Ile Tyr Ser
 280 260 265 270
 282 Asn Leu Ser Glu Ala Ser Pro Ala Leu Gly Arg Gln Ala Gly Thr Asn
 283 275 280 285
 285 Gly Gly Phe Ser Leu Asp His Ser Gly Ile Pro Ala Gln Asp Gln Tyr
 286 290 295 300
 288 His Asp Leu Arg Ser Asn Ser Pro Tyr Gly Ile Pro Gln Ser Pro Ala
 289 305 310 315 320
 291 Ser Leu Gln Ala Leu Pro Gly His Gln Pro Leu Ile Ser Ser Leu Val
 292 325 330 335
 294 Tyr Pro Asp Ser Gly Leu Gly Ile Met Gly Gln Gly Gly Gln Gly Val
 295 340 345 350
 297 Pro Gln Ser Met Arg Val Leu Ala Gly Asn Gly Pro Ser Ser Asp Leu
 298 355 360 365
 300 Ser Thr Gly Ser Ser Gly Gly Tyr Pro Asp Phe Pro Ala Ser Pro Ala
 301 370 375 380
 303 Ser Trp Leu Asp Glu Val Asp His Ala Gln Phe
 304 385 390 395
 307 <210> SEQ ID NO: 5
 308 <211> LENGTH: 394
 309 <212> TYPE: PRT
 310 <213> ORGANISM: Xenopus laevis
 312 <400> SEQUENCE: 5
 313 Met Leu Leu Glu Arg Val Arg Thr Gly Thr Gln Lys Ser Ser Asp Met
 314 1 5 10 15
 316 Cys Gly Tyr Thr Gly Ser Pro Glu Ile Pro Gln Cys Ala Gly Cys Asn
 317 20 25 30
 319 Gln His Ile Val Asp Arg Phe Ile Leu Lys Val Leu Asp Arg His Trp
 320 35 40 45
 322 His Ser Lys Cys Leu Lys Cys Asn Asp Cys Gln Ile Gln Leu Ala Glu
 323 50 55 60
 325 Lys Cys Phe Ser Arg Gly Asp Ser Val Tyr Cys Lys Asp Asp Phe Phe
 326 65 70 75 80
 328 Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys Gln Gln Gly Ile Pro Pro
 329 85 90 95
 331 Thr Gln Val Val Arg Arg Ala Gln Glu Phe Val Tyr His Leu His Cys
 332 100 105 110
 334 Phe Ala Cys Ile Val Cys Lys Arg Gln Leu Ala Thr Gly Asp Glu Phe
 335 115 120 125
 337 Tyr Leu Met Glu Asp Ser Arg Leu Val Cys Lys Ala Asp Tyr Glu Thr
 338 130 135 140
 340 Ala Lys Gln Arg Glu Ala Glu Ser Thr Ala Lys Arg Pro Arg Thr Thr
 341 145 150 155 160
 343 Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys Asn Ala Tyr Asn Asn Ser



Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/932,367A

DATE: 02/13/2002

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Input Set : A:\053844-5003.txt

Output Set: N:\CRF3\02132002\I932367A.raw

L:472 M:283 W: Missing Blank Line separator, <400> field identifier
L:473 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:477 M:283 W: Missing Blank Line separator, <400> field identifier
L:478 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:980 M:283 W: Missing Blank Line separator, <400> field identifier
L:981 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:985 M:283 W: Missing Blank Line separator, <400> field identifier
L:986 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:1319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1602 M:283 W: Missing Blank Line separator, <400> field identifier
L:1603 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (30) SEQUENCE:
L:1620 M:283 W: Missing Blank Line separator, <400> field identifier
L:1621 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (32) SEQUENCE: